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COLON TUMOR SPECIFIC BINDING PEPTIDES

This application claims priority to U.S. Provisional Application Serial Number 60/369,850 filed April 5, 2002 which is hereby incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

Colon carcinogenesis is thought to be a stepwise process that involves the transition of normal colon epithelium to neoplasm. The multistep progression of the disease requires years and possibly decades, and therefore apparently provides ample time for diagnosis and treatment. Unfortunately, however, 63% of colon cancer remains undetected until it has spread to the surrounding organs or lymph, a finding that correlates with a poor prognosis. In the gastrointestinal tract, conventional endoscopic techniques do not provide sufficient contrast for sensitive and reliable identification of early tumor disease.

One of the earliest recognizable events in the transition of normal colon epithelial cells into a carcinoma is the alteration of the cell kinetic processes of proliferation, differentiation, and apoptosis within the epithelial cells comprising the colon crypt. The zone of proliferation expands and ultimately encompasses the entire crypt. Moreover, the level of apoptosis is reduced and cannot balance the increased proliferation that occurs. The expansion of the proliferation zone is thought to result in the formation of a polyp that is composed of poorly-differentiated colonocytes and represents an intermediate stage in the development of a carcinoma. The transformation to carcinoma often is characterized by acquisition of an invasive phenotype wherein defective cells invade the underlying basement membrane.

Recent research has shed light on the genetic events that accompany the progression of normal colonic epithelium to neoplasm. In approximately 85% of sporadic colon cancers

and in all inherited cases of familial adenomatous polyposis (FAP) forms of colon cancer have mutated adenomatous polyposis coli, APC. Further, in both sporadic tumors and FAP, mutations in APC were identified at the earliest stages of neoplasia, aberrant crypt foci . These findings suggest that defects in the APC gene are the initiating event in the onset of the majority of colon tumors. In fact, APC appears to control colonic cell kinetics and seems to be involved in the first steps of colon carcinogenesis, particularly in the transition from normal to hyperproliferative coloncytes.

In light of the role played by the APC gene during colon tumorigenesis, it would be helpful to understand the functions of the APC protein. The APC protein is a large multidomain protein with many protein-protein interaction domains. It has been shown that APC binds to β-catenin, a protein that functions in cell adhesion and Wnt-based signal transduction. More than 90% of APC gene mutations inactivate the gene, resulting in premature termination of the transcript and subsequent truncation of the APC protein. Truncated APC proteins often retain the ability to dimerize and bind β-catenin, but lose the capacity to phosphorylate and alter intracellular levels of β-catenin and to bind to the microtubule cytoskeleton.

The failure of β-catenin levels to be properly regulated by proteasome degradation, and the subsequent increase of β-catenin-TCF complex formation results in an alteration of gene transcription. Functional β-catenin-TCF binding sites have been identified in the promoters of the cell cycle regulatory genes, cyclin D1 and c-myc and the overexpression of APC protein has been shown to block the cell cycle progression from the g0 and g1 phases to the s phase. Therefore, APC protein appears to have an important role in the regulation of colonic cell proliferation. Thus, the inactivation of the APC gene appears to disrupt both cell-cell and cell-matrix interaction, leading to inappropriate proliferation.

Through genetics, clinicians are able to identify patients that have an inherent risk for developing colon cancer. Although clinicians and researchers have identified an underlying molecular cause of colon cancer, this knowledge has translated into modest clinical success in the early diagnosis and treatment of colon cancer. Early work has focused on the use of antibodies for tumor recognition and drug delivery. However, when antibodies are used as the targeting molecule, the immunogenicity and long plasma half-life of these proteins were detrimental.

Currently, colon cancer detection methods are limited to recognition of relatively large abnormalities by visual inspection. Improved detection sensitivity through the use of diagnostic tools--such as high affinity peptides that exploit the molecular differences between normal, well-differentiated colonocytes and poorly-differentiated tumor cells--would be desirable.

It is apparent, therefore, that new methods that allow the accurate and convenient detection of neoplasms would dramatically extend life expectancy of many patients through disease prevention and are greatly to be desired. In particular, improved early detection methods that exploit the molecular differences between normal, well-differentiated colonocytes and neoplastic, poorly-differentiated colonocytes are highly desirable. Moreover, new methods of treating colon tumors are greatly to be desired.

SUMMARY OF THE INVENTION

Accordingly, it is an object of the invention to provide molecules that are selective or specific for colon tumors.

It is another object of the invention to provide molecules that exhibit decreased or a substantially nonexistent immunogenicity in an in vivo system.

These and other objects of the invention are provided for below.

In a compositional sense, the invention provides a peptide that selectively binds to colon cancer cells, the peptide preferably is a cyclic peptide. The peptide has the formula: A-X1-X2-X3-X4-X5-X6-X7-X8-X9-B,

wherein X1-X9 each are an amino acid, wherein A and B are absent or are amino acids or peptides containing up to 6 amino acids, and wherein amino acids X2, X3, X4, and X5 may be the same or different and each optionally may be absent. Preferably, the peptide is cyclic and is made up of the sequence cys-pro-ile-glu-asp-arg-pro-met-cys, where the peptide contains a disulfide bond between the cys side chains.

In a methodological sense, the invention provides a method of diagnosing the presence of colon tumor cells in a patient. This method contains the steps of contacting a sample of colon cells obtained from the patient with a diagnostic composition of the invention, and detecting binding of the composition to colon tumor cells. The invention also provides methods of treating a patient suffering from colon cancer, comprising steps of administering to the patient a pharmaceutical composition of the invention.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows the maturation of pool of peptides displayed on phage that binds selectively to HT29 cells.

Figure 2 shows selective binding of the phage pool to HT29 cells.

Figure 3 shows evolution of the sequences obtained from successive rounds of maturation on HT29 cells.

Figure 4 shows the dependence of HT29 binding on the presence of three amino acids, RPM, and their position within the peptide.

Figure 5 shows binding data demonstrating that phage displaying peptides containing the RPM motif bind selectively and specifically to HT29 cells.

Figure 6 shows immunofluorescence data demonstrating that peptides containing the RPM motif bind selectively to HT29 cells.

Figure 7 shows data demonstrating that binding of peptides containing the RPM motif to HT29 cells is stereospecific and that binding can be eliminated after protease treatment of the cells.

Figure 8 shows that a peptide containing the RPM motif localizes to the cell surface at 4°C and is internalized at 37 °C.

Figure 9 shows immunofluorescence data demonstrating that a peptide containing the RPM motif binds to colon tumors.

Figure 10 shows that a peptide containing the RPM motif does not bind to normal lung, liver or stomach or to liver or lung cancer.

Figure 11 shows that a peptide containing the RPM motif conjugated to a cytotoxic agent can kill colon tumor cells.

DETAILED DESCRIPTION

The invention provides peptides that selectively bind to colon tumor cells, relative to normal colon cells, as well as methods for obtaining the same. Accordingly, peptides of the invention can be used in any number of contexts, e.g. to diagnose the presence of colon tumor cells in patient samples, and to treat colon cancer.

Identification of certain colon tumor specific peptides:

The display of peptide libraries on the surface of bacteriophages was used to identify peptides with the desired binding properties.

The conventional use of phage display is to identify peptides that bind to homogenous target molecules in vitro. In an extension of phage display technology, Pasqualini & Ruoslahti, Nature 380:364-66 (1996), have reported the selection of peptides on a heterogeneous molecular population in the vasculature using in vivo phage display. Although the targeted endothelial cells of vasculature have a mixture of cell surface proteins with different affinities and conformations, injecting mice with peptide phage libraries led to the identification of specific peptides for these targets. Through this approach, peptides have been identified that "home" to vascular tissue.

Although peptides have been identified that bind to tissue specific vasculature, this in vivo phage display technique cannot be used to identify peptides that bind to cancer cells, as the phage are confined to the vasculature, i.e. where cancer cells are not. However, the present inventors surprisingly found that established cancer cell lines and "normal" cell lines could be use to obtain cancer cell specific peptides in vitro. Selection of cancer-specific peptides and their epitopes using peptide phage display libraries is a powerful method that allows direct identification of peptides that can be used for the diagnosis and treatment of colon cancer.

The role of phage display in the discovery of new drugs and diagnostics has been exemplified by the use of peptides identified by Pasqualini & Ruoslahti, supra, in conjunction with PET scan imaging of tumors and their use to selectively deliver toxins to cancer cells. When cell selective peptides are coupled to the apoptotic agent, TNFα, the efficacy:toxicity ratio of the coupled TNF was 14 times greater than with TNF alone.

In order to identify potential diagnostics and therapeutics for neoplastic colonocytes, the present inventors used phage display to generate peptide libraries that distinguish between well-differentiated (HCT116) and poorly-differentiated colon carcinoma cells (HT29). The present inventors have developed a screening protocol that uses selection and subtraction on intact, viable cells, resulting in phage libraries that exhibit high binding selectivity for the poorly-differentiated HT29 cells. This approach allowed identification of peptides that are selective and specific for tumor cells, rather than cells of the vasculature.

Analysis of the selected library resulted in the identification of a nine amino acid, disulfide-constrained peptide having a three amino acid (arg-pro-met) motif (herein designated an "RPM" peptide) that specifically binds HT29 cells. Binding specificity was confirmed by showing that an RPM peptide successfully abolished binding of RPM-bearing phage to HT29 cells. In contrast, an unrelated peptide failed to block the RPM-phage binding. A majority of the sequences recovered after selection contained the RPM tripeptide motif directly adjacent to the C-terminal cysteine.

Further investigation proved that the binding of RPM to HT29 cells was not simply the result of non-specific charge interactions. In particular, a peptide synthesized with all D amino acids failed to compete for binding to the cells. Likewise, a peptide containing an RPM sequence in the middle of the peptide instead of adjacent to the C-terminus failed to compete for binding to HT29 cells. These data prove that binding to HT29 cells was dependent on the peptide sequence and not the phage proteins or non-specific interactions.

RPM was confirmed to be a functional consensus sequence by synthesizing alanine substitution mutants in the RPM sequence and determining their ability to compete for binding with wild type RPM. Mutating either the arginine or methionine to alanine resulted in an impaired ability of that sequence to compete for binding, while mutating the proline to an alanine resulted in a complete abrogation of the peptide's ability to compete. Further,

moving the RPM motif to the middle of the peptide abolished the ability of that peptide to compete with the wild type RPM peptide, suggesting that the cysteine plays a role in RPM binding to HT29 cells.

In further confirmation studies, immunohistochemical staining using FITC-conjugated RPM peptide showed binding of RPM to tumor tissue from four patients. Adjacent normal tissue showed no binding of FITC-conjugated RPM. Once again, binding studies revealed that labeled RPM peptide competed with unlabeled RPM peptide, but not an unrelated peptide. In addition, RPM failed to stain a panel of non-colon tissues including lung, liver and stomach. The translation of the RPM peptide selectivity from colon cancer cell lines to human colon cancer was unexpected. Typically, immortalized cell lines seldom recapitulate the in vivo setting.

The inability of an all D amino acid RPM peptide to compete for phage binding to HT29 cells and the sensitivity of RPM binding to HT29 cells treated with proteases indicated that RPM recognizes a colon tumor specific cell surface protein.

Peptides of the Invention:

The peptides of the present invention offer a great benefit by circumventing the shortcomings of conventional diagnostic and treatment modalities, such as the use of antibodies, in that they are non-immunogenic or substantially non-immunogenic and combine high affinity and selectivity with more desirable pharmocokinetic properties than previously known drugs or proteins. The peptides contemplated by the invention provide an added benefit for tumor targeting by virtue of their ability to selectively deliver therapeutic agents, such as cytotoxic agents, to the tumor. Specific targeting using high affinity and high selectivity peptides permits use of low doses of anti-tumor agents, thereby eliminating or diminishing the toxic effects of conventional chemotherapeutics, such as doxorubicin.

The peptides of the invention generally can be represented by the formula:

A-X1-X2-X3-X4-X5-X6-X7-X8-X9-B,

where X1-X9 each are an amino acid, and where A and B are absent or are amino acids or peptides containing up to 6 amino acids. Amino acids X2-X5 may be absent.

The peptides according to the invention are, therefore, relatively short, typically containing up to 15 amino acids. The skilled artisan will recognize, however, that the peptides may contain as few as 5 amino acids and as many as 21. The skilled worker also will recognize that a peptide of the invention will contain any number of amino acids between 9 and 21, such as 10, 12, 14, 16, 18 and 20 amino acids.

In one embodiment, the peptides contain a central cyclic nonapeptide motif, where the peptide is cyclized via the side chains of X1 and X9. When A and B are absent, the peptide may be cyclized via formation of a lactam between the amino and carboxyl functions of X1 and X9. In a specific embodiment, X1 and X9 are both cysteine, and the peptide is cyclized via the formation of a disulfide bond between the two cysteine side chains.

In another embodiment, the peptides are represented by the above formula and contain a cyclic nonapeptide motif, where:

X1 and X9 are cys;

X2 is pro, ala, val, asp, gln, phe, or ile;

X3 is ile, leu, glu, met, pro, or his;

X4 is glu, asp, his, arg, pro, ala, lys, gln, or ser;

X5 is asp, glu, ser, phe, gln, met, val;

X6 is arg, his, gln, phe, ser, pro;

X7 is pro, tyr, arg, or trp; and

X8 is met, ser, leu, or arg.

In another embodiment, the peptides contain a cyclic nonapeptide motif, where X1 and X9 are cys, X6-X8 are arg-pro-met, and X2 is pro, ala, val, asp, gln, phe, or ile; X3 is ile,

leu, glu, met, pro, or his; X4 is glu, asp, his, arg, pro, ala, lys, gln, or ser; and X5 is asp, glu, ser, phe, gln, met, val.

In another embodiment, the peptides contain a cyclic nonapeptide motif, where X1 and X9 are cys, X6-X8 are arg-pro-met, X2 is pro; X3 is ile or leu; X4 is glu, asp, or arg; and X5 is asp or glu. In another embodiment, the peptides contain a cyclic nonapeptide motif, where X1-X9 is cys-pro-ile-glu-asp-arg-pro-met-cys. In each of the embodiments where X1 and X9 are cys, the peptide is cyclized via a disulfide bond between the side chains of X1 and X9. In yet another embodiment, the peptide contains a arg-pro-met-cys motif, which may be constrained in a cyclic structure, wherein the cys-side chain forms a disulfide bond with another cysteine side chain located elsewhere in the peptide.

In yet further embodiments, X1 and X9 are cys, and X2-X8 are selected, respectively, from the group consisting of:

ALLPNKT	AQPLKQN	SMSSHRW	APSQRAQ	AYPYWLY	SNSQDQN
ELNAAHT	DHPVPWR	SPQSQPM	ETGYSFR	DLREHTL	SRLDSPF
ETLSPRD	DRIGARQ	SYDYAKH	FESQSRL	FESQSRL	THLMPLT
FMKTLSN	GTATLHW	TKSLLLA	HQLYRGL	HDSLYRA	TSPLPSQ
IQGSGST	HNPPRPQ	TSSTPKA	KASMKSP	HNVRFPN	TTRGPST
KATAMNS	HQSSPQL	VSLQPMT	LAHASNS	HQTNPNE	VSNQIAN
LAKVPAS	HSSHTHQ	VTTLNLT	MLPHGRT	IDPSLGL	NFNSRAS
IHPVPWR	NGTSRIQ	KAESPME	NLKQPEH	KATMTAT	NRALHSY
KDKDNLP	NSARWSV	KLVPTHQ	NSHDPEN	KNERAYL	NSKDPGT
KNLTHKH	NVTWGDT	KPTLPLS	PATPLKF	KQHHVTE	PKGSGMN
KQPTSNY	PNQGAYV	KSPSSLQ	PPAHHPN	KTPIPKI	QLPRSQS
KTTHPAL	QQSLSLI	LHMHQHI	QTPSLRL	LKQHWYS	SAHHPHA
LLPLAAP	SHQDPSL	LPHSQAH	SLSQPFR	LPSKFSH	SSRPPWN

LSASTLM	THSHKKP	LSPISLQ	TNPMRLH	LTPEPQY	TQLPVSW
NASLMSV	TTWWAST	NATQWQH	VHKFKPF	NGSYVWR	NPNSNDM
NSMPLHA	NWQPATH	PFGMVHT	PHPWPGK	PKMLGAA	PLTPTTV
PPHTLGL	PQELHPN	PSNETTQ	PSTAELA	PSYSTSY	PVSNLLQ
QPPMFYS	QPQSQPM	QTTPPFL	QWAALRP	and SLRTAAA.	

Mixtures or pools of the peptides in any combination may be used, but the invention also contemplates the use of a single type of peptide.

In the context of the present invention, a peptide is "selective" for binding to tumor cells when it binds at least about twice as strongly to tumor cells as to normal cells. A peptide is "specific" for binding to tumor cells when it binds about 5-10 times more strongly to tumor cells as to normal cells. Methods for measuring relative binding affinities are well known in the art.

As will be apparent by the following text, the invention contemplates the formulation of diagnostic and therapeutic compositions containing one or more peptides of the invention. Accordingly, the invention provides diagnostic compositions that contain a mixture of peptides, each of which can be conjugated to a detectable label, such as a radioactive or fluorescent marker. A peptide of the invention also can be conjugated to a detectable peptide moiety capable of specifically interacting with and/or being specifically bound by, another peptide or molecule. To this end, the detectable moiety may be a moiety such as a biotin molecule (which can bind to streptavidin), a peptide epitope that can be recognized and bound by a binding agent such as an antibody, (for example a FLAG peptide, to which a commercially available anti-flag antibody can bind), a Jun or Fos moiety (which are able to interact with each other) or any other epitope that is specifically recognized by a binding reagent, such as an antibody. Suitable conjugation moieties are well known in the art.

In addition, the invention contemplates pharmaceutical preparations, which contain a composition of peptides and a pharmaceutically acceptable sterile vehicle, carrier or excipient therefor. By "sterile" is meant a vehicle, carrier or excipient that does not bring about an intolerable immunogenic response when administered to a subject.

Therapeutic and Diagnostic Methods of the Invention:

Due to their properties, one or more peptides of the invention can, accordingly, be used in any number of methodologies. In particular, one or more peptides of the invention can be employed for diagnosis and/or treatment of disease. Thus, the invention provides methods of diagnosing the presence of colon tumor cells in a patient comprising the steps of administering to the paitent an effective amount of a diagnostic composition contemplated herein. The administered composition would, accordingly, bind to the colon tumor cells, and this binding can be detected by the presence of a detectable moiety, as described herein. By "effective amount" of a diagnostic composition is the amount needed to allow the skilled worker to determine if a patient is suffering from colon cancer.

The peptides of the invention also can find use in detecting the presence of tumors other than colon tumors. For example, the skilled worker will appreciate that certain peptides of the invention can be selective or specific for colon-derived tumors in other tissues or organs.

In the diagnostic setting, peptides of the present invention may be used to image or detect the presence of tumor cells in patients, either in vivo or ex vivo samples. Thus, for example, the peptide may be conjugated to (e.g., produced as a fusion protein with) a detectable label, such as a fluorescent dye or a radioactive label, to allow detection of peptide binding to a tumor cell taken as a biopsy. Methods of labeling peptides for this purpose are well known in the art. A peptide of the invention also can be produced as a fusion with an alternative detection moiety, as further described herein, e.g. biotin, FLAG, jun, fos or an

epitope recognized by an antibody. Methods for detecting labeled peptides in vitro and in vivo also are well known in the art.

A peptide of the invention also may be conjugated with a therapeutic moiety for use in treating colon cancer. Suitable therapeutic moieties include, for example, cytotoxic drugs, such as drugs that interfere with intracellular protein synthesis, toxins, including toxins that lack an intact cell-binding domain, and radioactive moieties. Other therapeutic agents that can be linked to the peptide are known in the art. Drugs that interfere with intracellular protein synthesis are known to these skilled in the art and include puromycin, cycloheximide, and ribonuclease.

Toxins useful as therapeutics are known to those skilled in the art and include plant and bacterial toxins, such as, abrin, alpha toxin, diphtheria toxin, exotoxin, gelonin, pokeweed antiviral protein, ricin, and saporin. Toxins in their native form require a minimum of three different biochemical functions to kill cells: a cell binding function, a cytotoxic function, and a function to translocate the toxic activity into the cells. The modified toxins used in the present invention differ from native toxins in that the domain providing the cell binding function of the native toxin is nonfunctioning because the domain is missing partially or totally.

The drug or modified toxin is then treated by methods known to those skilled in the art to permit them to be conjugated to the protein containing at least one mercapto group. Methods for treating toxins and, in particular, modified Pseudomonas exotoxins, are disclosed in Batkra et al., Proc. Natl. Acad. Sci. USA, Vol. 86, pp. 8545-8549, 1989; Seetharam et al., The Journal of Biol. Chem., Vol. 266, No. 26, pp. 17376-17381, 1991; and Pastan et al., U.S. Pat. No. 4,892,827, all incorporated herein by reference. A preferred modified Pseudomonas exotoxin comprises ADP ribosylating activate, an ability to

translocate across a cell membrane and devoid of a functional receptor binder region Ia of the native toxin. One such modified Pseudomonas exotoxin is devoid of amino acids 1-252 and 365-380 of native Pseudomonas exotoxin and contains a -KDEL mutation instead of -REDLK at the carboxyl terminus.

Peptides of the invention also are amenable to non-invasive methods for diagnosing tumors. Due to the ongoing sloughing off of cells in the colon, fecal material is likely to contain colon cells. A sample of fecal material, accordingly, could be prepared for screening with a peptide of the invention, on the basis that said peptide would specifically or selectively bind to an tumor cell contained in the feces.

With regard to therapeutic approaches, it previously has been shown that conjugating drugs to peptides specific for angiogenesis markers could eliminate tumors by destroying their vasculature (see U.S. Patent No. 6,491,894). Despite such advance, however, anti-cancer therapy focused in the vasculator is ineffective against many tumors under 1mm^3, which are able to exist in isolation from the vasculature by receiving their nutrients from adjacent normal blood vessels. Accordingly, therapy limited to the vasculature leaves the task of eliminating at least some portion of the tumor remaining.

Thus, another use of peptides of the invention (e.g., those isolated according to phage display selection methods described herein) is the coupling of peptides to cell toxins for therapeutic or treatment purposes, namely, to treat patients suffering from colon cancer. In this regard, the invention provides a process which entails administering the peptides in a form conjugated to a therapeutic agent, such as a cytotoxic moiety. The peptide binds to tumor cells in the patient and delivers the therapeutic agent selectively or specifically to those cells. Suitable therapeutic agents and methods of conjugating such agents to peptides are well known in the art.

Indeed, the present inventors have generated a reagent that can eliminate a tumor (including the remains of tumor not in contact with the vasculature) by binding selectively to cancer cells and, by being internalized, by carrying a toxin to the cells. In vitro, HT29 colon cancer cells were selectively killed by incubating them with RPM conjugated to a toxin. In contrast, HCT116 (non tumor) cells were not affected by treatment with RPM-$(KLAK)_2$. This demonstrates an exquisite selectivity of RPM for HT29 cells, as well as the utility and promise of this approach for selectively destroying tumor cells while leaving normal cells intact or substantially unharmed. The peptide was shown to be internalized upon binding to the tumor cells.

Methods of identifying further colon-specific peptides:

Other features contemplated by the invention include methods of identifying a homing molecule that homes to a marker on a colon tumor cell. The method includes the steps of contacting in vitro a substantially purified population of tumor cell lines (e.g., HT29 colon cancer cells) with one or more molecules and determining the specific binding of a molecule to the tumor cell vis-à-vis a non-neoplastic colon cell (e.g., HCT116), where the presence of specific binding identifies the molecule as a homing molecule that homes to a colon tumor cell.

Further homing molecules that home to a colon tumor can be identified by screening one or more molecules, for example, a library of molecules. As used herein, the term "library" means a collection of molecules. A library can contain a few or a large number of different molecules, varying from about ten molecules to several billion molecules or more.

Methods for preparing libraries containing diverse populations of various types of molecules such as peptides, peptoids and peptidomimetics are well known in the art and various libraries are commercially available (see, for example, Ecker and Crooke, Biotechnology 13:351-360 (1995), and Blondelle et al., Trends Anal. Chem. 14:83-92 (1995),

and the references cited therein, each of which is incorporated herein by reference; see, also, Goodman and Ro, Peptidomimetics for Drug Design, in "Burger's Medicinal Chemistry and Drug Discovery" Vol. 1 (ed. M. E. Wolff; John Wiley & Sons 1995), pages 803-861, and Gordon et al., J. Med. Chem. 37:1385-1401 (1994), each of which is incorporated herein by reference). Where a molecule is a peptide, protein or fragment thereof, the molecule can be produced in vitro directly or can be expressed from a nucleic acid, which can be produced in vitro. Methods of synthetic peptide and nucleic acid chemistry are well known in the art.

A library of molecules also can be produced, for example, by constructing a cDNA expression library from mRNA collected from a cell, tissue, organ or organism of interest. Methods for producing such libraries are well known in the art (see, for example, Sambrook et al., Molecular Cloning: A laboratory manual (Cold Spring Harbor Laboratory Press 1989), which is incorporated herein by reference). Preferably, a peptide encoded by the cDNA is expressed on the surface of a cell or a virus containing the cDNA. For example, cDNA can be cloned into a phage vector such as fuse 5 (Example I), wherein, upon expression, the encoded peptide is expressed as a fusion protein on the surface of the phage.

The following working examples are illustrative embodiments of the invention are and do not, therefore, limit the invention.

EXAMPLES

Materials and Methods

Generation of HS-1. An aliquot (10 ul) of the C7C complete phage library from New England Biolabs (Beverley, MA) was incubated with $2x10^5$ cells HT29 cells at 4C for 45 minutes in PBS with 0.5 % BSA (binding buffer). After incubation, cells were washed with PBS/0.5% BSA/0.05% Tween (wash buffer) for a total of 6 washes. Phage that bound were eluted with 0.2M glycine (pH 2.2) for 8 minutes then neutralized with 50 uL of 1M Tris-HCl (pH 9.0). After elution, phage were PEG-NaCl precipitated then resuspended in 300 uL of

binding buffer and incubated with $2.0x10^5$ HCT116 cells at 4°C for 45 minutes a total of 5 incubations (steps 2-6). The phage that did not bind to the HCT116 cells were amplified (step 7) then incubated with 2x 10^5 HT29 cells as above. Cells were washed to remove unbound phage and the bound phage was eluted. The number of phage bound was determined and the remaining eluate was amplifed. The amplified phage was used with the same number of HT29 cells and the process was repeated (steps 9-12) for a total of five rounds of maturation. After the five rounds of selection, phage from each round was titered, plaques were picked, phage DNA amplified by PCR and finally, sequenced.

Synthesis of Peptides

Phage binding assay. HT29 cells were incubated with peptide in binding buffer at concentrations of 0, 0.1, 1, 10, 100, or 1000 μM for 30 minutes at 4°C. After 30 minutes of incubation, 10^{10} pfu of phage were added to the cells and incubated at 4°C for an additional 45 minutes. Following incubation, cells were washed 6x with wash buffer and the phage remaining bound were eluted with glycine. The number of phage bound to the cells was quantified with real time PCR.

Immunohistochemistry

Cell Culture: HT29, HCT116, or a 50% mixture of HT29 and HCT116 cells were plated on glass slides (Nalge). Wells were incubated with 10 μM of RPM-FITC peptide for 45 minutes at 4°C or 37°C. After washing with wash buffer, cells were blocked with 1% NGS, 0.1% BSA, 0.1% Triton-X100 in PBS. Following the blocking step, wells were incubated with the polyclonal p53 antibody, D01, (Santa Cruz) for 1 hour at room temperature. The wells were washed and incubated with the secondary antibodies GαFITC Alexa 488 (Molecular Probes) and GαMouse Alexa 647 (Molecular Probes) and the nuclear

stain Topro-3 (Molecular Probes). Wells were washed and mounted using Pro-Long Anti-fade (Molecular Probes). Slides were analyzed by confocal microscopy.

Primary Tissue Analysis

A biopsy of sporadic colon adenocarcinoma, liver and lung sarcoma, and grossly uninvolved colon, liver, lung, and stomach were frozen in optimum cutting temperature (OCT) and 5-μM-thick cryostat sections placed on glass slides. Sections were stained with H&E and untreated adjacent sections were incubated with RPM-FITC. After incubating with RPM-FITC in binding buffer for 45 minutes at 4°C, slides were washed and mounted using Pro-Long Anti-Fade (Molecular Probes). Nuclei were visualized by a quick incubation with Topro-3 (Molecular Probes) present in the last wash. Samples were analyzed by confocal microscopy.

Protease Assay

HT29 cells were incubated at 37°C with either active or boiled Collagenase diluted 1:20 for 10 minutes, Trypsin-EDTA 0.25% (Gibco) for 5 minutes or Proteinase K (Gibco) diluted 1:600 for 1 minute. After incubation, cells were then incubated with RPM bearing phage as described above. The number of phage remaining bound was quantified by real time PCR.

RPM-KLAK and KLAK on HT29 and HCT116 cells. HT29 and HCT116 cells were incubated with increasing log concentrations of RPM-KLAK or KLAK for 72 hours at 37°C. After incubation, MTT was added to a final concentration of 2.5 ug/mL and incubated at 37°C for 1 hour. The media/MTT was removed carefully and the cells dissolved with 0.1N HCl in isopropanol. Absorbance was read on a plate reader (Cytofluor II, Perceptive Biosystems) at 570 nm.

Results

HS-1 library is selective for HT29 cells and contains a consensus binding motif. To identify potential molecular markers of colorectal cancer, phage display was used to generate peptide libraries that distinguish between well-differentiated (HCT116) and poorly-differentiated (HT29) colon carcinoma cells. In addition to having characteristics of poorly-differentiated tumor colonocytes, another distinguishing feature of HT29 cells is that the adenomatous polyposis coli (APC) gene, which is mutated in approximately 85% of colon cancers, is also mutated in HT29 cells. In contrast, HCT116 colon cancer cells contain wild-type APC. To identify cell surface proteins present only on HT29 cells, the present inventors used an M13 random, disulfide constrained, peptide phage display library, C7C, to select on cells at conditions (4°C) that should inhibit internalization of the phage. Secreted and cell surface proteins are important among protein targets because they are useful as both diagnostic markers and targets for drug delivery. The mature HT29 cell selective library was named HS-1.

After generation of the HS-1 library, the effectiveness of the maturation scheme for generating a HT29 selective library was determined by testing the library for its ability to bind HT29 and HCT116 cells. A constant number of phage from the amplified pool of each round was incubated with HT29 or HCT116 cells and the number of phage present in the acid elution was quantified (figure 1a). After the initial round of maturation and subtraction, the number of phage binding to HT29 and HCT116 cells was equivalent. Following amplification and the second round of selection, a two-fold selectivity of the library for HT29 cells was evident. Maximum selectivity (ten-fold) of the library for HT29 cells occurred after the third round of selection and did not increase with further selection steps.

To demonstrate that the original phage library was unbiased toward the sequence RPM, phage from the first round of maturation were sequenced. RPM was absent from the

sequences of the phage isolated from round 1. Two rounds of maturation showed the emergence of the RPM peptide with 4 out of 25 phage containing the RPM sequence. Nevertheless, round 2, similar to round 1, lacked a clear consensus sequence. Next, individual phage plaques from selection rounds 3 and 4, which were the rounds of maximal selectivity for HT29 cells, were isolated, and the DNA from each phage plaque was amplified by PCR then sequenced. Peptide sequences were compiled and analyzed for homology using Megalign alignment software. Despite the theoretical complexity of 10^9 sequences in the starting population, a clear majority, 20/27, (figure 1B, rounds 3 and 4) expressed an identical peptide motif, RPM. Moreover, in round 3, 24 out of 27 phage and in round 4, 25 out of 27 phage contained at least the amino acids PM (figure 1B). Of the sequences examined, the RPM sequence was always found directly adjacent to the C-terminal cysteine.

RPM peptide binding to HT29 cells is selective and mediated through the peptide sequence.

The enrichment of peptides with the RPM sequence suggested that binding to HT29 cells depended on the peptide displayed by the phage and not on an incidental property of the phage. To determine whether CPIEDRPMC displaying phage bind to HT29 cells specifically, a competition assay was performed using phage and synthetic peptides, peptides corresponding to the specific sequence, CPIEDRPMC, and the non-specific sequence, CKHLGPQLC, were synthesized by standard methods and oxidized to form a disulfide bond. Reaction of the peptides before and after oxidation with Ellman's reagent was performed to verify presence of the disulfide bond. CKHLGPQLC was isolated from a previous screen for peptides that bound to HT29 cells and as such bound to HT29 cells. In figure 2A, HT29 cells were incubated with increasing log concentrations of CPIEDRPMC peptide and with a constant number of either specific or non-specific phage. The number of phage binding to the HT29 cells was quantified and the percentage binding calculated based on the number of phage that bind in the absence of competitor. The sequence CPIEDRPMC was competed

with specific competitor but not with the non-specific competitor. Specific competitor reduced the level of RPM associated binding to HT29 cells to less than 4% whereas the level of binding to HT29 cells remained constant at 100% in the presence of non-specific competitor (Figure 2A). The reciprocal experiment was also done with HT29 cells incubated with increasing log concentrations of specific or non-specific peptide and a constant concentration of phage displaying the peptide CPIEDRPMC. The results are similar to what was observed in figure 2A in that a peptide sequence corresponding to CPIEDRPMC was able to compete phage bearing the same sequence but a peptide sequence CKHLGPQLC was not able to compete phage bearing the CPIEDRPMC sequence.

The peptide then was tested to determine whether it was able to differentiate HT29 from HCT116 cells. In order to distinguish HT29 from HCT116 cells in our immunohistochemical assays, staining was carried out in the presence of the transcription factor, p53. Staining for the protein p53 is a way to visually discriminate HT29 from HCT116 cells, since p53 is mutated and accumulates in HT29 cells but is wild type in HCT116 cells and thus, is rapidly degraded. As expected, immunohistochemical analysis of HT29 and HCT116 cells for p53 demonstrated a differential staining of HT29 and HCT116 cells with high levels of p53 expression detected in HT29 cells (Figure 2B). To test the ability of the fluorescein conjugated peptide (RPM-FITC) to preferentially bind HT29 cells, HT29 and HCT116 cells were stained with RPM-FITC. After incubation for 1 hour at 4°C with RPM-FITC, the HT29 cells showed fluorescence whereas the HCT116 cells exhibited little or no fluorescence (Figure 2B). When a mixture of HT29 and HCT116 cells was incubated with RPM-FITC and concurrently analyzed for the presence of p53, cells with the highest level of p53 protein also bound RPM-FITC (Figure 5A).

To determine whether RPM-FITC binding to HT29 cells was dependent on the peptide sequence, a competition assay was performed. HT29 cells were incubated with

RPM-FITC and unlabeled specific or non-specific competitor. Specific competitor was able to abolish RPM-FITC staining of HT29 cells while RPM-FITC binding was unaffected by the presence of non-specific competitor.

RPM binds to human colon tumors but not to normal colon lung, liver, or stomach, or to liver or lung cancer.

Since the above data suggested that RPM was selective and specific for HT29 cells, it was determined whether RPM was able to bind and differentially stain human colon tumor as opposed to normal colon. A peptide-binding assay performed on frozen sections prepared from a biopsy sample of human colon tumor and grossly uninvolved normal colon showed the preferential binding of RPM-FITC to human colon tumor (Figure 3). Tumors from four different patients were stained and all showed a staining pattern similar to that in figure 3 (data not shown). The ability of unlabeled specific competitor to abrogate binding to colon tumor shows that binding of RPM-FITC to colon tumor was mediated by RPM.

To determine whether RPM-FITC was able to bind cancers originated from tissues other than colon or to other normal tissues, a peptide-binding assay was performed on cryostat sections of lung and liver cancer, and grossly uninvolved lung, liver, and stomach. As a positive control, a section of colon tumor was stained in parallel with the other sections. Figure 4 shows that lung and liver cancer as well as grossly uninvolved lung, liver, and stomach showed no labeling with RPM-FITC. In contrast, colon tumor exhibited bright staining when incubated with RPM-FITC.

Binding to HT29 cells is dependent on the amino acids, RPMC-C.

The ability of the peptide to bind selectively to human colon tumors was intriguing and prompted characterization of the interaction of the peptide with HT29 cells. The phage selection procedure produced naturally occurring substitution mutants so the phage and the peptide could be used to determine a functional consensus sequence for the family. HT29

cells were incubated with increasing log concentrations of CPIEDRPMC peptide and a constant number of phage displaying one of the sequences were selected. The kinetics of competition were almost identical (within 2 fold) for the phage displaying the RPM motif. In contrast, the phage bearing the peptide sequence PM was competed at a 40 fold lower concentration of peptide than the phage bearing the RPM motif. The identity of the 4 residues before the RPM motif were unimportant and did not effect the ability of the peptide to compete with the phage for binding to HT29 cells.

The above assay narrowed the functional consensus sequence to RPM. To examine the importance of each residue within the RPM sequence for binding to HT29 cells, peptides were synthesized having alanine mutations in either the arginine, proline, or methionine residue and used in phage competition assay as described above. Mutations in the arginine or methionine had the same effect on the ability of peptide to compete an RPM displaying phage (Figure 5B). The EC50 of competition shifted by ~100 fold from 5 uM with an RPM peptide to 690 and 545 uM using either the APM or RPA peptide. The peptide with the proline to alanine mutation was not able to compete with phage binding to HT29 cells at even 1mM of peptide.

Since all of the peptides isolated from the selection contained the RPM motif at the C-terminal end of the peptide directly adjacent to the final cysteine, the importance of the cysteines for RPM binding activity was examined. A peptide was prepared bearing the RPM motif in the middle of the peptide (RPM middle), CPIRPMEDC, and used in the phage competition assays. Figure 5C shows that the (RPM) middle peptide was over 100 fold less potent when compared to RPM in competing with the phage for HT29 cell binding.

RPM peptide binding to HT29 cells is consistent with binding to a HT29 protein.

Since protein-protein interactions typically depend on the chiral nature of the amino acids, an all D amino-acid RPM peptide was used in phage competition assay to try to

determine if RPM was binding to a HT29 protein. HT29 cells were incubated with increasing log concentrations of either All D RPM or RPM and a constant number of RPM phage. After incubation, washing, and acid elution, the number of phage remaining bound was quantified. Figure 6A shows that the binding of RPM to HT29 cells was dependent on the chiral nature of the amino acids since a RPM peptide consisting of all D amino acids was not able to compete with RPM phage for binding to HT29 cells.

The above data suggested that RPM was binding to a HT29 protein. In order to further this observation, HT29 cells were treated with active or boiled proteases to determine the effect of treatment on the ability of an RPM displaying phage to bind. HT29 cells were treated with active or boiled collagenase for 15 minutes, trypsin for 5 minutes, or proteinase K for 0.5 minutes at 37°C. After protease treatment, cells were washed, then an equal number of phage were added and allowed to bind. Quantification of the number of phage bound to the cells after protease treatment revealed that the ability of phage to bind to any of the active protease treated cells was decreased by 85, 90, and 90%(Figure 6B). The decrease in phage binding to the HT29 cells was due to the protease activity since boiling the proteases abolished the effect with phage binding returning to levels of that observed for PBS treated cells (Figure 6B). Treating the cells with proteases did not affect cell viability. After treating HT29 cells with proteases as described above, MTT was added to the cells and incubated for 45 minutes at 37°C. After incubation, the cells were solubilized with 0.1N HCl in isopropanol and the absorbance due to MTT incorporation was determined. The treated cells had an average absorbance of 0.188 (PBS), 0.189 (collagenase), 0.175 (trypsin), and 0.183 (proteinase K).

RPM is internalized and able to selectively deliver a toxin to HT29 cells.

The ability of a molecule to translocate across the cell membrane is important for drug delivery. HT29 cells were incubated for 1 hour at either 4°C or 37°C in the presence of 100

uM RPM-FITC. After incubation, cells were washed, fixed with 2% paraformaldehyde, then incubated with an anti-FITC secondary antibody to amplify the fluorescence signal. When the cells were incubated with RPM-FITC at 4°C, peptide binding was confined to the cell surface of the HT29 cells. In contrast, incubating HT29 cells with RPM-FITC at 37°C revealed the presence of diffuse staining throughout the cells.

Since RPM-FITC is internalized at 37°C, RPM may be used to deliver a toxin to HT29 cells. To demonstrate this, an antimicrobial toxin, $(KLAK)_2$, was used that selectively disrupts the mitochondrial membrane of eukaryotic cells while the cytoplasmic membrane remains intact. Cells that were incubated with $(KLAK)_2$ alone or with free peptide were refractory to death induced by the toxin. However, when a peptide that was specific and also internalized by cells was conjugated to $(KLAK)_2$, the cells were killed. RPM was coupled to $(KLAK)_2$ and incubated with HT29 and HCT116 cells with either $(KLAK)_2$ alone as a negative control or RPM-$(KLAK)_2$. Cells were treated for 72 hours at 37°C. At the end of the incubation, cell viability was measured by MTT assay. As expected, incubation of either cell line with $(KLAK)_2$ did not effect the viability of the cells (Figure 7B). Since RPM should not bind to HCT116 cells, HCT116 cells should be resistant to death induced by RPM-$(KLAK)_2$. This was indeed observed for HCT116 incubation with RPM $(KLAK)_2$ (Figure 6B). In contrast, HT29 cell viability was affected by incubation with RPM-$(KLAK)_2$ in a concentration dependent manner with an LC50 of 0.31 uM.